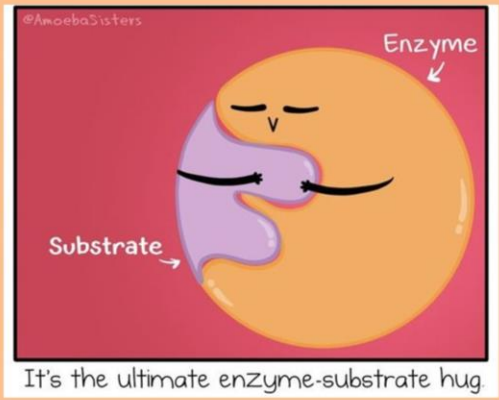
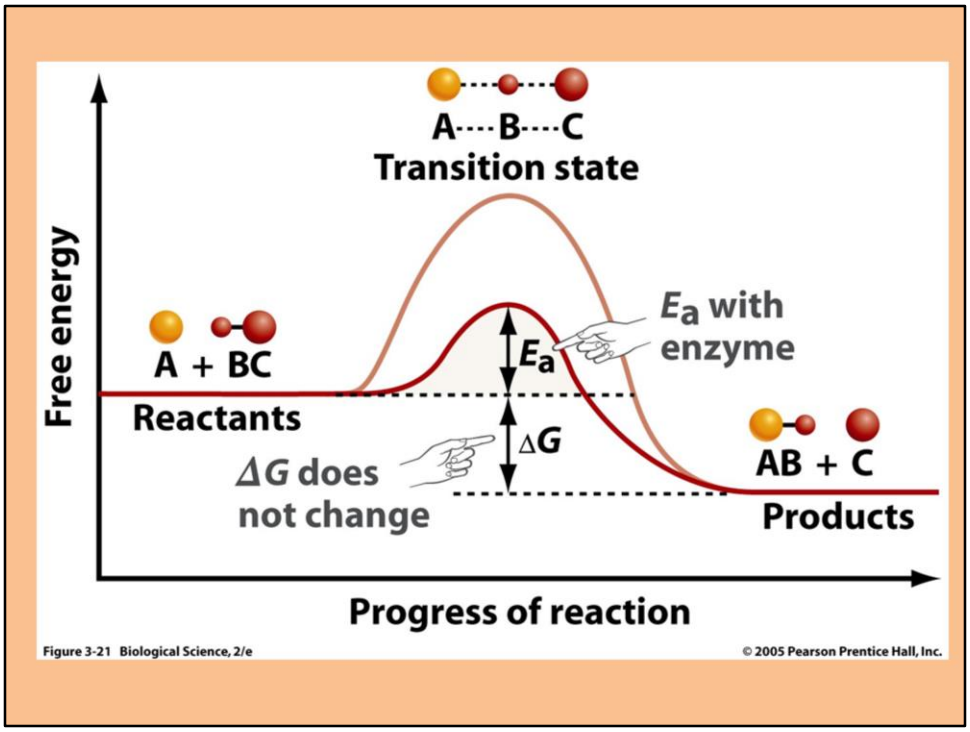
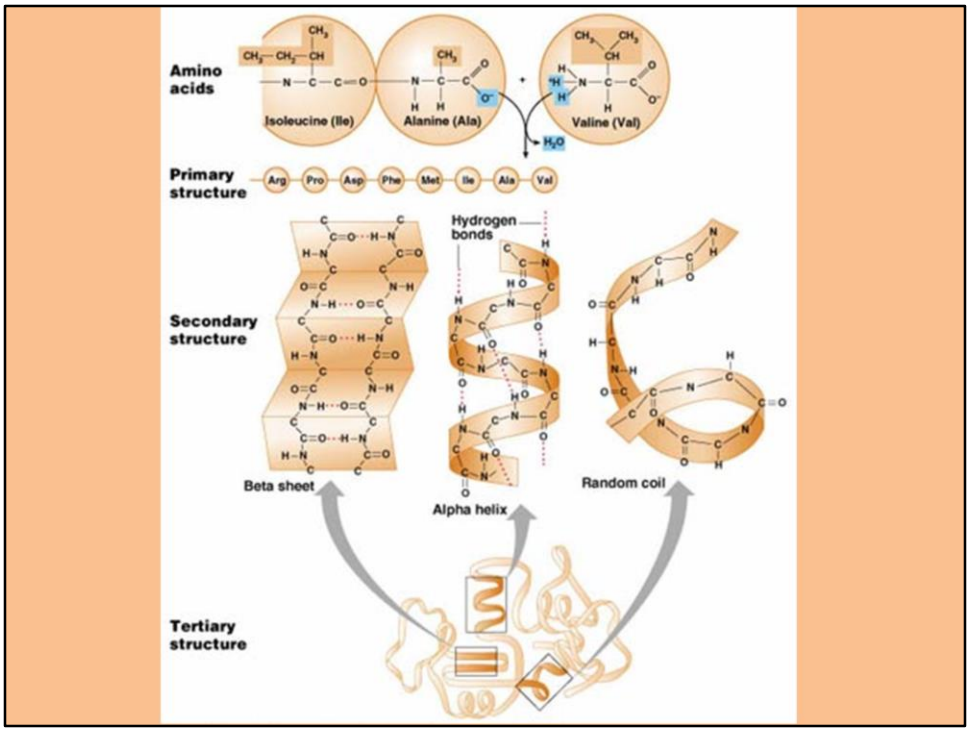
Enzymes


@AmoebaSisters
Enzyme
Substrate
It's the ultimate enzyme-substrate hug.



Enzymes DO change the Ea by allowing transition state to be reached much more quickly.

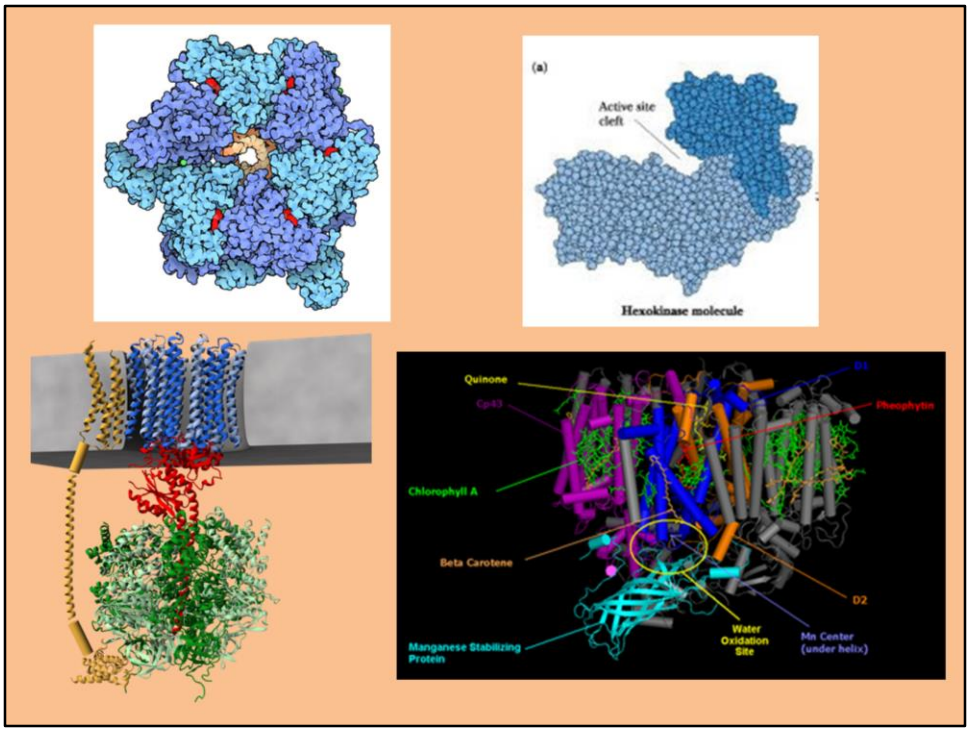
Enzymes DO NOT change the energy of the substrates, products or overall change in energy (ΔG)



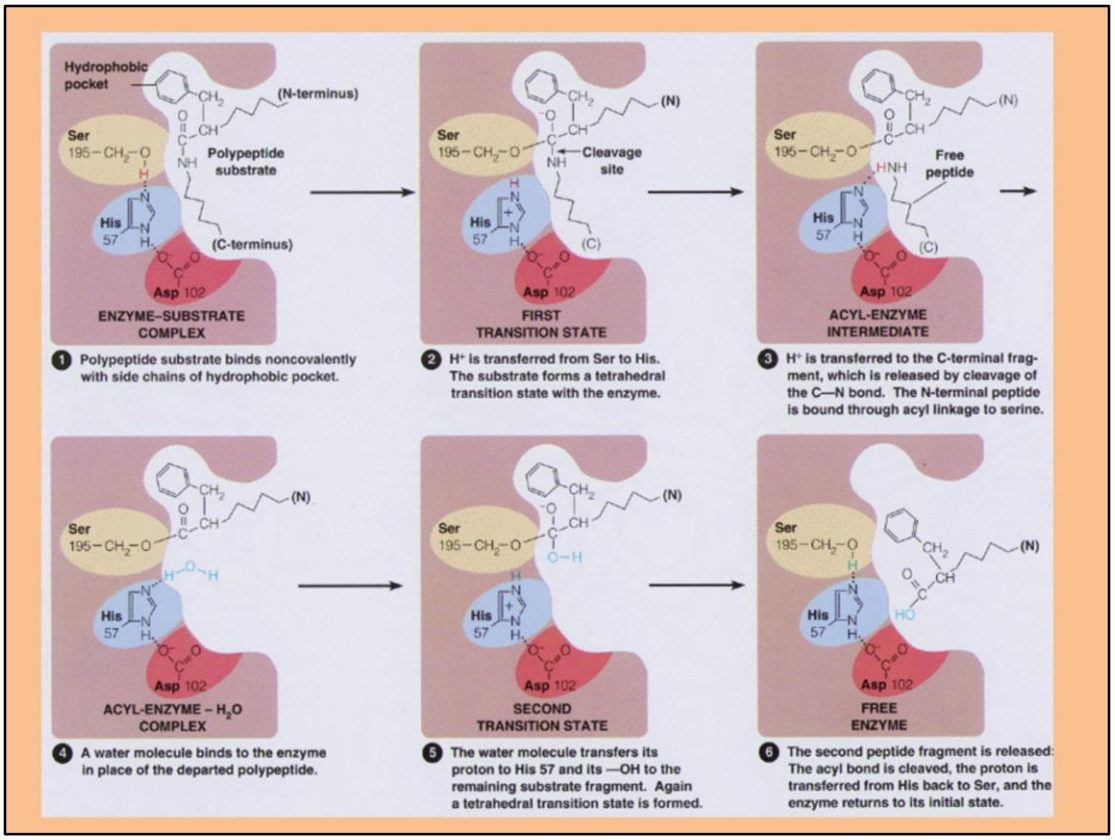
Primary structure: The sequence of amino acids determined by a gene. Formed by peptide bonds.

Secondary structure: Individual coils & folds held together by hydrogen bonds between nearby amino acids.

Tertiary structure: The overall 3D form of the polypeptide held together by many bond types (covalent, hydrogen, ionic).



Overall structure of protein enzymes depend on bonds being held at specific places. This is determined by an enzymes: Amino acid sequence determined by the coding genes.

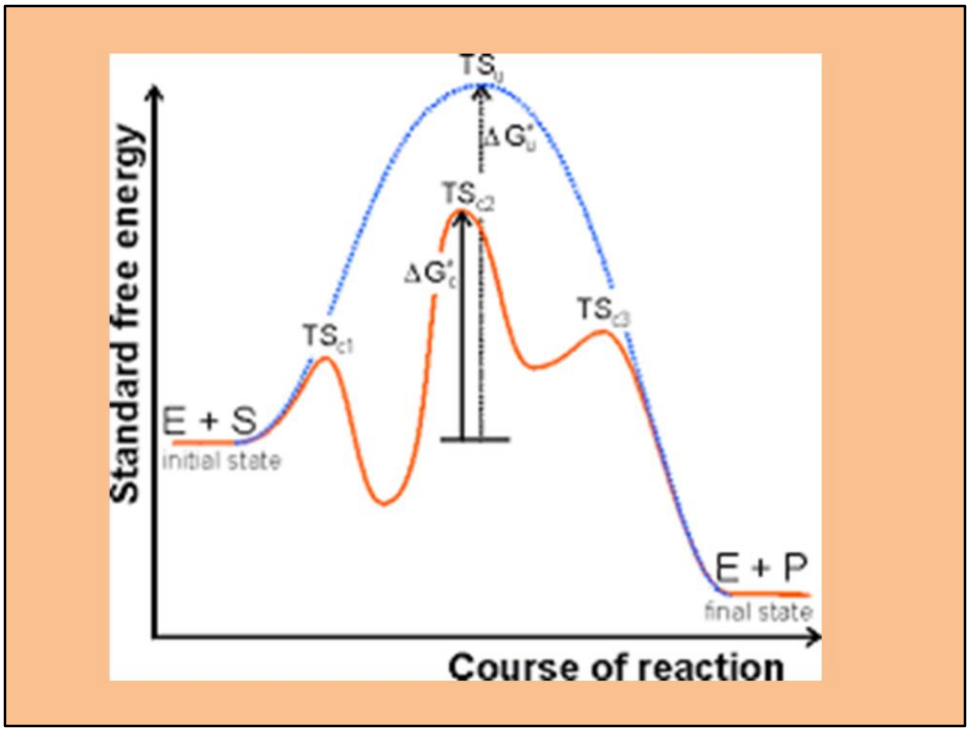


The Active Site & Mechanisms of Enzyme Action

1. Favorable initial binding interactions draw substrates in.
2. Unstable bonds formed, make likely to react (change).

The active site's catalytic properties are determined by its amino acids & their interactions with other nearby molecules.

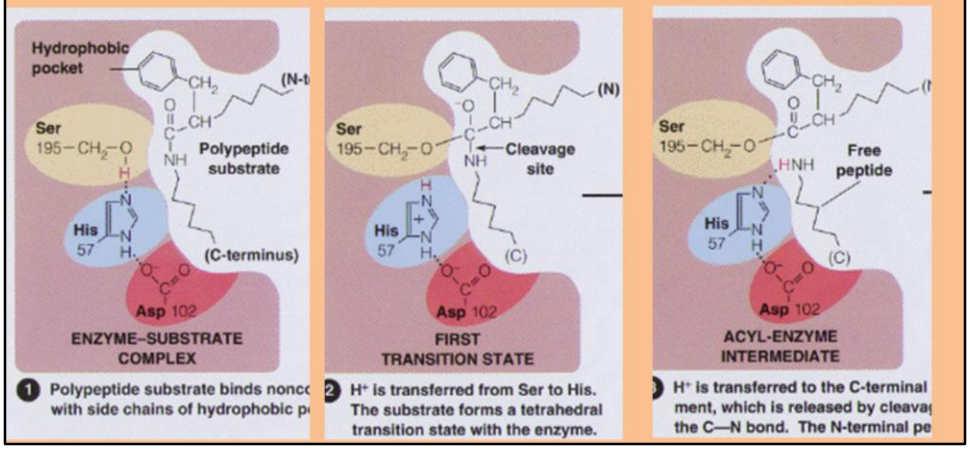
Some enzymes are very specific, others very generic.



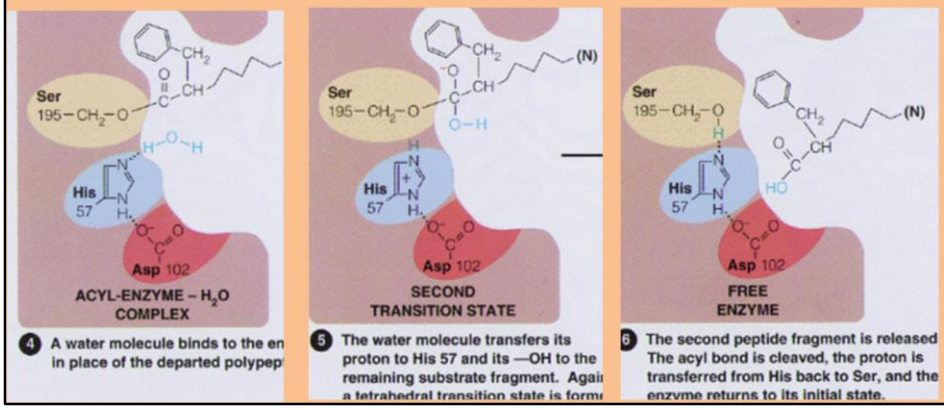
Reaction without enzyme takes longer because: Substrate does not have enough energy to reach the transition state.

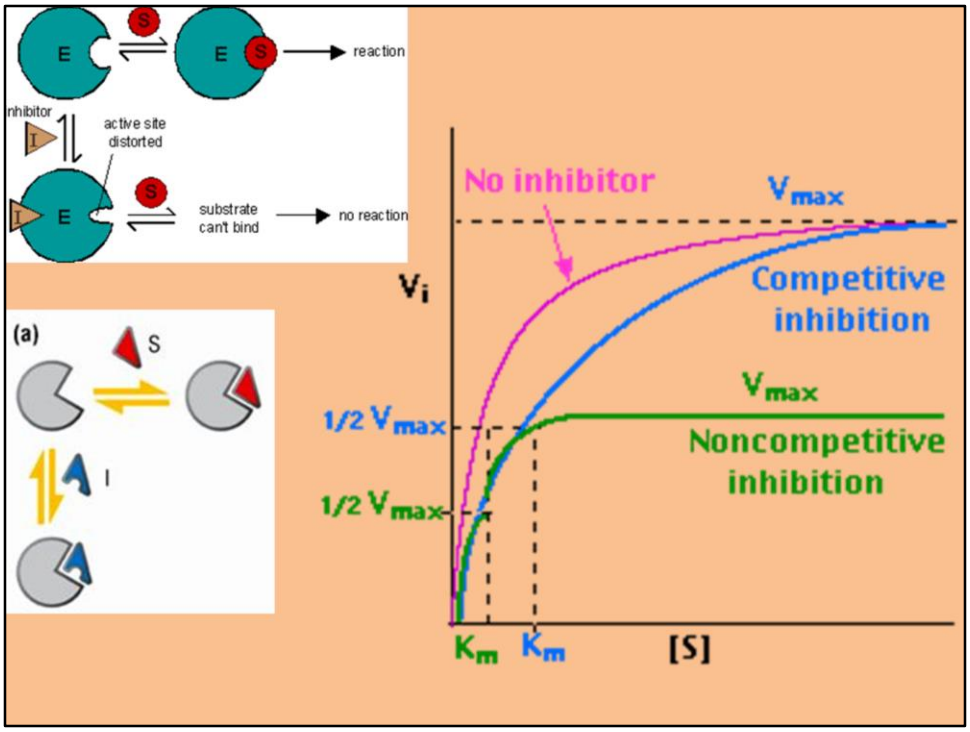
Enzymes lower Ea by: making substrates unstable, thus more likely to change.

- **High Temperature**: deform hydrogen bond between Ser & His, enzyme denatures (Step 1).
- **Bases**: Selectively remove & add H+ to themselves. Cause H+ to transfer from Ser to itself rather than to His. Interferes with reaction rate (Step 2).



- **Salts**: Bond strongly to other charged atoms. In His + state (step 5) a salt could bind irreversibly, making enzyme nonfunctional.
- **Acids**: Release H+. Instead of His & Asp re-hydrogen bonding, released H+ from an acid could bond with O- on Asp, changing the active site shape & reactivity.

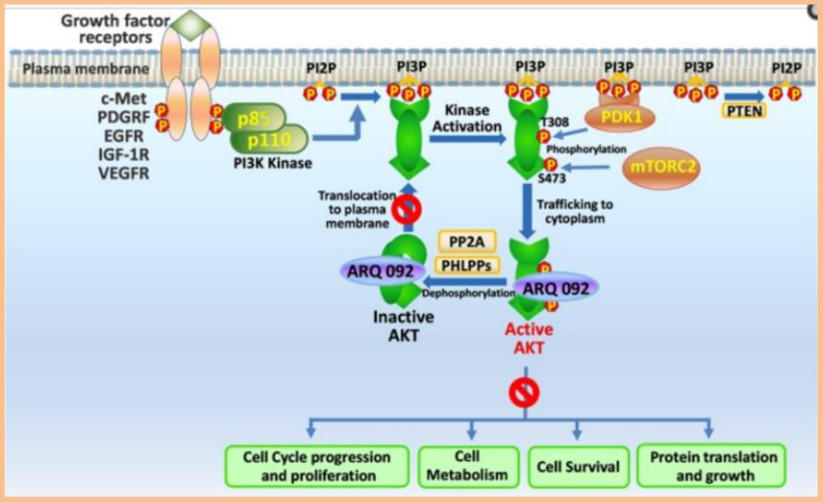




Competitive Inhibition: Inhibitor blocks active site directly but doesn't interfere with enzyme's ability to work. Rate depends on amount of substrate available.

Non- Competitive Inhibition: Inhibition alters active site & results in many non-functional enzymes. Rate depends on available functional enzymes.

Allosteric inhibition to treat cancer cells: **Miransertib** experimental cancer medication allosterically inhibits specific active kinases without causing many other downstream effects (stimulating other processes also leading to cancer as with some other drugs).



Allosteric regulation in metabolism